

ence Range: 1 to 6200

10	20	30	40	50	60	70
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
GACGGATCGG	GAGATCTCCC	GATCCCCTAT	GGTCGACTCT	CAGTACAATC	TGCTCTGATG	CCGCATAGTT
80	90	100	110	120	130	140
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
AAGCCAGTAT	CTGCTCCCTG	CTTGTGTGTT	GGAGGTCGCT	GAGTAGTGCG	CGAGCAAAAT	TTAAGCTACA
150	160	170	180	190	200	210
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
ACAAGGCAAG	GCTTGACCGA	CAATTGCATG	AAGAATCTGC	TTAGGGTTAG	GCGTTTTGCG	CTGCTTCGCG
220	230	240	250	260	270	280
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
ATGTACGGGC	CAGATATACG	CGTTGACATT	GATTATTGAC	TAGTTATTAA	TAGTAATCAA	TTACGGGGTC
290	300	310	320	330	340	350
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
ATTAGTTCAT	AGCCCATATA	TGGAGTTCGG	CGTTACATAA	CTTACGGTAA	ATGGCCCGCC	TGGCTGACCG
360	370	380	390	400	410	420
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
CCCAACGACC	CCCGCCATT	GACGTCAATA	ATGACGTATG	TTCCCATAGT	AACGCCAATA	GGGACTTTCC
430	440	450	460	470	480	490
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
ATTGACGTCA	ATGGGTGGAC	TATTTACGGT	AAACTGCCCA	CTTGGCAGTA	CATCAAGTGT	ATCATATGCC
500	510	520	530	540	550	560
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
AAGTACGCCC	CCTATTGACG	TCAATGACGG	TAAATGGCCC	GCCTGGCATT	ATGCCCAGTA	CATGACCTTA
570	580	590	600	610	620	630
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
TGGGACTTTC	CTACTTGGCA	GTACATCTAC	GTATTAGTCA	TCGCTATTAC	CATGGTGATG	CGGTTTTGGC
640	650	660	670	680	690	700
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
AGTACATCAA	TGGGCGTGGA	TAGCGGTTTG	ACTCACGGGG	ATTTCCAAGT	CTCCACCCCA	TTGACGTCAA
710	720	730	740	750	760	770
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
TGGGAGTTTG	TTTTGGCACC	AAAATCAACG	GGACTTTCCA	AAATGTCGTA	ACAACTCCGC	CCCATTGACG
780	790	800	810	820	830	840
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
CAAATGGGCG	GTAGGCGTGT	ACGGTGGGAG	GTCTATATAA	GCAGAGCTCT	CTGGCTAACT	AGAGAACCCA
850	860	870	880	890	900	910
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
CTGCTTAACT	GGCTTATCGA	AATTAATACG	ACTCACTATA	GGGAGACCCA	AGCTTCGCAG	AATTCCTGCG
920	930	940	950	960	970	980
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
GCTGCTACAG	TGTGTCCAGC	GTCCTGCCTG	GCTGTGCTGA	GUGCTGGAAC	AGTGGCGCAT	CATTCAAGTG
990	1000	1010	1020	1030	1040	1050
* * * *	* * * *	* * * *	* * * *	* * * *	* * * *	* * * *
CACAGTTACC	CATCCTGAGT	CTGGCACCTT	AACTGGCACA	ATTGCCAAAG	TCACAGGTGA	GCTCAGATGC

FIGURE 1

1060 1070 1080 1090 1100 1110 1120
* * * * * * *
ATACCAGGAC ATTGTATGAC GTTCCCTGCT CACATGCCTG CTTTCTTCCT ATAATACAGA TGCTCAACTA

1130 1140 1150 1160 1170 1180 1190
* * * * * * *
ACTGCTCATG TCCTTATATC ACAGAGGGAA ATTGGAGCTA TCTGAGGAAC TGCCCAGAAG GGAAGGGCAG

1200 1210 1220 1230 1240 1250 1260
* * * * * * *
AGGGGTCTTG CTCTCCTTGT CTGAGCCATA ACTCTTCTTT CTACCTTCCA GTGAACACCT TCCCACCCCCA

1270 1280 1290 1300 1310 1320 1330
* * * * * * *
GGTCCACCTG CTACCGCCGC CGTCGGAGGA GCTGGCCCTG AATGAGCTCT TGTCCCTGAC ATGCCTGGTG

1340 1350 1360 1370 1380 1390 1400
* * * * * * *
CGAGCTTTCA ACCCTAAAGA AGTGCTGGTG CGATGGCTGC ATGGAAATGA GGAGCTGTCC CCAGAAAGCT

1410 1420 1430 1440 1450 1460 1470
* * * * * * *
ACCTAGTGTT TGAGCCCCTA AAGGAGCCAG GCGAGGGAGC CACCACCTAC CTGGTGACAA GEGTGTTGCG

1480 1490 1500 1510 1520 1530 1540
* * * * * * *
TGTATCAGCT GAAAGCTTGA TATCGAATC CGGAGGCCGA ACCGGCAGTG CAGCCCGAAG CCCC GCAGTC

1550 1560 1570 1580 1590
* * * * *
CCCCGAGCAGC CGTGGCC ATG CGT CCC CTG CGC CCC CGC GCC GCG CTG CTG GCG CTC CTG
Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu>
_ _ a _ _ a _ _ a _ _ a _ ORF RF[1] _ _ a _ _ a _ _ a _ _ a _ >

1610 1620 1630 1640 1650
* * * * *
GCC TCG CTC CTG GCC GCG CCC CCG GTG GCC CCG GCC GAG GCC CCG CAC CTG GTG CAT
Ala Ser Leu Leu Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val His>
_ _ a _ _ a _ _ a _ _ a _ ORF RF[1] _ _ a _ _ a _ _ a _ _ a _ >

1660 1670 1680 1690 1700 1710
* * * * * *
GTG GAC GCG GCC CGC GCG CTG TGG CCC CTG CGG CGC TTC TGG AGG AGC ACA GGC TTC
Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg Ser Thr Gly Phe>
_ _ a _ _ a _ _ a _ _ a _ ORF RF[1] _ _ a _ _ a _ _ a _ _ a _ >

1720 1730 1740 1750 1760 1770
* * * * * *
TGC CCC CCG CTG CCA CAC AGC CAG GCT GAC CAG TAC GTC CTC AGC TGG GAC CAG CAG
Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr Val Leu Ser Trp Asp Gln Gln>
_ _ a _ _ a _ _ a _ _ a _ ORF RF[1] _ _ a _ _ a _ _ a _ _ a _ >

1780 1790 1800 1810 1820
* * * * *
CTC AAC CTC GCC TAT GTG GGC GCC GTC CCT CAC CGC GGC ATC AAG CAG GTC CGG ACC
Leu Asn Leu Ala Tyr Val Gly Ala Val Pro His Arg Gly Ile Lys Gln Val Arg Thr>
_ _ a _ _ a _ _ a _ _ a _ ORF RF[1] _ _ a _ _ a _ _ a _ _ a _ >

1830 1840 1850 1860 1870 1880
* * * * * *
CAC TGG CTG CTG GAG CTT GTC ACC ACC AGG GGG TCC ACT GGA CGG GGC CTG AGC TAC
His Trp Leu Leu Glu Leu Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr>

Abstract

P. 31

FIGURE 1A

2460 2470 2480 2490 2500 2510
* * * * * *
GCG GAC CCG CTG GTG GGC TGG TCC CTG CCA CAG CCG TGG AGG GCG GAC GTG ACC TAC
Ala Asp Pro Leu Val Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr>
_ _ _ _ _ ORF RF[1] _ _ _ _ _>

2520 2530 2540 2550 2560
* * * * *
GCG GCC ATG GTG GTG AAG GTC ATC GCG CAG CAT CAG AAC CTG CTA CTG GCC AAC ACC
Ala Ala Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn Thr>
_ _ _ _ _ ORF RF[1] _ _ _ _ _>

2570 2580 2590 2600 2610 2620
* * * * * *
ACC TCC GCC TTC CCC TAC GCG CTC CTG AGC AAC GAC AAT GCC TTC CTG AGC TAC CAC
Thr Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe Leu Ser Tyr His>
_ _ _ _ _ ORF RF[1] _ _ _ _ _>

2630 2640 2650 2660 2670 2680
* * * * * *
CCG CAC CCC TTC GCG CAG CGC ACG CTC ACC GCG CGC TTC CAG GTC AAC AAC ACC GCG
Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg Phe Gln Val Asn Asn Thr Arg>
_ _ _ _ _ ORF RF[1] _ _ _ _ _>

2690 2700 2710 2720 2730
* * * * *
CCG CCG CAC GTG CAG CTG TTG CGC AAG CCG GTG CTC ACG GCC ATG GGG CTG CTG GCG
Pro Pro His Val Gln Leu Leu Arg Lys Pro Val Leu Thr Ala Met Gly Leu Leu Ala>
_ _ _ _ _ ORF RF[1] _ _ _ _ _>

2740 2750 2760 2770 2780 2790
* * * * * *
CTG CTG GAT GAG GAG CAG CTC TGG GCC GAA GTG TCG CAG GCC GGG ACC GTC CTG GAC
Leu Leu Asp Glu Glu Gln Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp>
_ _ _ _ _ ORF RF[1] _ _ _ _ _>

2800 2810 2820 2830 2840 2850
* * * * * *
AGC AAC CAC ACG GTG GGC GTC CTG GCC AGC GCC CAC CGC CCC CAG GGC CCG GCC GAC
Ser Asn His Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp>
_ _ _ _ _ ORF RF[1] _ _ _ _ _>

2860 2870 2880 2890 2900 2910
* * * * * *
GCC TGG CGC GCC GCG GTG CTG ATC TAC GCG AGC GAC GAC ACC CGC GCC CAC CCC AAC
Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala His Pro Asn>
_ _ _ _ _ ORF RF[1] _ _ _ _ _>

2920 2930 2940 2950 2960
* * * * *
CGC AGC GTC GCG GTG ACC CTG CGG CTG CGC GGG GTG CCC CCC GGC CCG GGC CTG GTC
Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro Pro Gly Pro Gly Leu Val>
_ _ _ _ _ ORF RF[1] _ _ _ _ _>

2970 2980 2990 3000 3010 3020
* * * * * *
TAC GTC ACG CGC TAC CTG GAC AAC GGG CTC TGC AGC CCC GAC GGC GAG TGG CGG CGC
Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu Cys Ser Pro Asp Gly Glu Trp Arg Arg>
_ _ _ _ _ ORF RF[1] _ _ _ _ _>

3030 3040 3050 3060 3070 3080
* * * * * *

FIGURE 1C

AAAAAAAAAA AAAAAAAAAAG AATTCCTGCA GCCCGGGGGA TCCACTAGTT CTAGAGGGCC CGTTTAAACC
 3760 3770 3780 3790 3800 3810 3820
 * * * * *
 CGCTGATCAG CCTCGACTGT GCCTTCTAGT TGCCAGCCAT CTGTTGTTTG CCCCTCCCCC GTGCCTTCCT
 3830 3840 3850 3860 3870 3880 3890
 * * * * *
 TGACCCTGGA AGGTGCCACT CCCACTGTCC TTCTCTAATA AAATGAGGAA ATTGCATCGC ATTGTCTGAG
 3900 3910 3920 3930 3940 3950 3960
 * * * * *
 TAGGTGTCAT TCTATTCTGG GGGGTGGGGT GGGGCAGGAC AGCAAGGGGG AGGATTGGGA AGACAATAGC
 3970 3980 3990 4000 4010 4020 4030
 * * * * *
 AGGCATGCTG GGGATGCGGT GGGCTCTATG GCTTCTGAGG CGGAAAGAAC CAGCTGGGGC TCGAGAGCTT
 4040 4050 4060 4070 4080 4090 4100
 * * * * *
 GGCGTAATCA TGGTCATAGC TGTTTCCTGT GTGAAATTGT TATCCGCTCA CAATTCCACA CAACATACGA
 4110 4120 4130 4140 4150 4160 4170
 * * * * *
 GCCGGAAGCA TAAAGTGTA AGCCTGGGGT GCCTAATGAG TGAGCTAACT CACATTAATT GCGTTGCGCT
 4180 4190 4200 4210 4220 4230 4240
 * * * * *
 CACTGCCCGC TTTCCAGTCG GGAAACCTGT CGTGCCAGCT GCATTAATGA ATCGGCCAAC GCGCGGGGAG
 4250 4260 4270 4280 4290 4300 4310
 * * * * *
 AGGCGGTTTG CGTATGCGC GCTCTTCCGC TTCCTCGCTC ACTGACTCGC TGCGCTCGGT CGTTCGGCTG
 4320 4330 4340 4350 4360 4370 4380
 * * * * *
 CGGCGAGCGG TATCAGCTCA CTCAAAGGCG GTAATACGGT TATCCACAGA ATCAGGGGAT AACGCAGGAA
 4390 4400 4410 4420 4430 4440 4450
 * * * * *
 AGAACATGTG AGCAAAAGGC CAGCAAAAGG CCAGGAACCG TAAAAGGCC GCGTTGCTGG CGTTTTTCCA
 4460 4470 4480 4490 4500 4510 4520
 * * * * *
 TAGGCTCCGC CCCCTGACG AGCATCACAA AAATCGACGC TCAAGTCAGA GGTGGCGAAA CCCGACAGGA
 4530 4540 4550 4560 4570 4580 4590
 * * * * *
 CTATAAAGAT ACCAGGCGTT TCCCCCTGGA AGCTCCCTCG TGCGCTCTCC TGTTCGACC CTGCCGCTTA
 4600 4610 4620 4630 4640 4650 4660
 * * * * *
 CCGGATACCT GTCCGCCTTT CTCCCTTCGG GAAGCGTGGC GCTTTCTCAA TGCTCAGCT GTAGGTATCT
 4670 4680 4690 4700 4710 4720 4730
 * * * * *
 CAGTTCGGTG TAGGTCGTTT GCTCCAAGCT GGGCTGTGTG CACGAACCCC CCGTTCAGCC CGACCGCTGC
 4740 4750 4760 4770 4780 4790 4800
 * * * * *
 GCCTTATCCG GTAACATCG TCTTGAGTCC AACCCGGTAA GACACGACTT ATCGCCACTG GCAGCAGCCA

FIGURE 1E

4810	4820	4830	4840	4850	4860	4870
* * *	* * *	* * *	* * *	* * *	* * *	* * *
CTGGTAACAG	GATTAGCAGA	GCGAGGTATG	TAGGCGGTGC	TACAGAGTTC	TTGAAGTGGT	GGCCTAACTA
4880	4890	4900	4910	4920	4930	4940
* * *	* * *	* * *	* * *	* * *	* * *	* * *
CGGCTACACT	AGAAGGACAG	TATTTGGTAT	CTGCGCTCTG	CTGAAGCCAG	TTACCTTCGG	AAAAAGAGTT
4950	4960	4970	4980	4990	5000	5010
* * *	* * *	* * *	* * *	* * *	* * *	* * *
GGTAGCTCTT	GATCCGGCAA	ACAAACCACC	GCTGGTAGCG	GTGGTTTTTT	TGTTTGCAAG	CAGCAGATTA
5020	5030	5040	5050	5060	5070	5080
* * *	* * *	* * *	* * *	* * *	* * *	* * *
CGCGCAGAAA	AAAAGGATCT	CAAGAAGATC	CTTTGATCTT	TTCTACGGGG	TCTGACGCTC	AGTGGAACGA
5090	5100	5110	5120	5130	5140	5150
* * *	* * *	* * *	* * *	* * *	* * *	* * *
AAATCACGT	TAAGGGATT	TGGTCATGAG	ATTATCAAAA	AGGATCTTCA	CCTAGATCCT	TTTAAATTAA
5160	5170	5180	5190	5200	5210	5220
* * *	* * *	* * *	* * *	* * *	* * *	* * *
AAATGAAGTT	TTAAATCAAT	CTAAAGTATA	TATGAGTAAA	CTTGGTCTGA	CAGTTACCAA	TGCTTAATCA
5230	5240	5250	5260	5270	5280	5290
* * *	* * *	* * *	* * *	* * *	* * *	* * *
GTGAGGCACC	TATCTCAGCG	ATCTGTCTAT	TTCGTTTCATC	CATAGTTGCC	TGACTCCCCG	TCGTGTAGAT
5300	5310	5320	5330	5340	5350	5360
* * *	* * *	* * *	* * *	* * *	* * *	* * *
AACTACGATA	CGGGAGGGCT	TACCATCTGG	CCCCAGTGCT	GCAATGATAC	CGCGAGACCC	ACGCTCACCG
5370	5380	5390	5400	5410	5420	5430
* * *	* * *	* * *	* * *	* * *	* * *	* * *
GCTCCAGATT	TATCAGCAAT	AAACCAGCCA	GCCGGAAGGG	CCGAGCGCAG	AAGTGGTCCT	GCAACTTTAT
5440	5450	5460	5470	5480	5490	5500
* * *	* * *	* * *	* * *	* * *	* * *	* * *
CCGCTCCAT	CCAGTCTATT	AATTGTTGCC	GGGAAGCTAG	AGTAAGTAGT	TCGCCAGTTA	ATAGTTTGCG
5510	5520	5530	5540	5550	5560	5570
* * *	* * *	* * *	* * *	* * *	* * *	* * *
CAACGTTGTT	GCCATTGCTA	CAGGCATCGT	GGTGTCACGC	TCGTCGTTTG	GTATGGCTTC	ATTCAGCTCC
5580	5590	5600	5610	5620	5630	5640
* * *	* * *	* * *	* * *	* * *	* * *	* * *
GGTCCCCAAC	GATCAAGGCG	AGTTACATGA	TCCCCCATGT	TGTGCAAAAA	AGCGGTTAGC	TCCTTCGGTC
5650	5660	5670	5680	5690	5700	5710
* * *	* * *	* * *	* * *	* * *	* * *	* * *
CTCCGATCGT	TGTCAGAAGT	AAGTTGGCCG	CAGTGTTATC	ACTCATGGTT	ATGGCAGCAC	TGCATAATTC
5720	5730	5740	5750	5760	5770	5780
* * *	* * *	* * *	* * *	* * *	* * *	* * *
TCTTACTGTC	ATGCCATCCG	TAAGATGCTT	TTCTGTGACT	GGTGAGTACT	CAACCAAGTC	ATTCTGAGAA
5790	5800	5810	5820	5830	5840	5850
* * *	* * *	* * *	* * *	* * *	* * *	* * *
TAGTGTATGC	GGCGACCGAG	TTGCTCTTGC	CCGGCTGCAA	TACGGGATAA	TACCGCGCCA	CATAGCAGAA
5860	5870	5880	5890	5900	5910	5920
* * *	* * *	* * *	* * *	* * *	* * *	* * *

FIGURE 1F

CTTTAAAAGT GTCATCATT GGAAAACGTT CTCGGGGCG AAAACTCTCA AGGATCTTAC CGCTGTTGAG

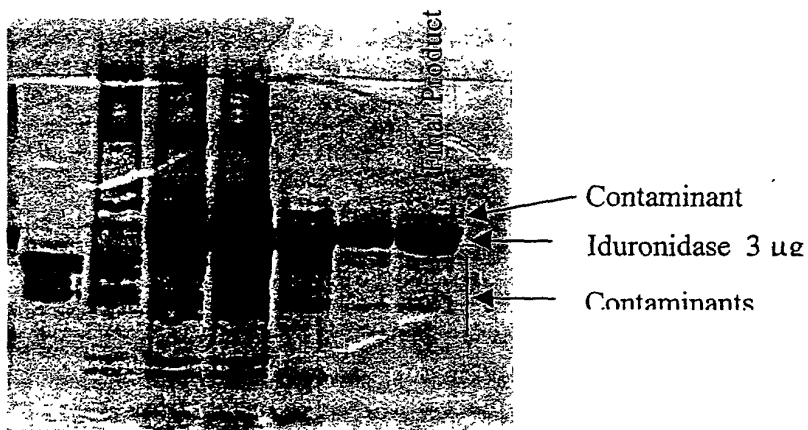
5930	5940	5950	5960	5970	5980	5990
* *	* *	* *	* *	* *	* *	* *
ATCCAGTTCG	ATGTAACCCA	CTCGTGCACC	CAACTGATCT	TCAGCATCTT	TTACTTTCAC	CAGCGTTTCT
6000	6010	6020	6030	6040	6050	6060
* *	* *	* *	* *	* *	* *	* *
GGGTGAGCAA	AAACAGGAAG	GCAAAATGCC	GCAAAAAAGG	GAATAAGGGC	GACACGGAAA	TGTTGAATAC
6070	6080	6090	6100	6110	6120	6130
* *	* *	* *	* *	* *	* *	* *
TCATACTCTT	CCTTTTCAA	TATTATTGAA	GCATTTATCA	GGGTTATTGT	CTCATGAGCG	GATACATATT
6140	6150	6160	6170	6180	6190	6200
* *	* *	* *	* *	* *	* *	* *
TGAATGTATT	TAGAAAAATA	AACAAATAGG	GGTTCCGCGC	ACATTTCCCC	GAAAAGTGCC	ACCTGACGTC

099344-11301

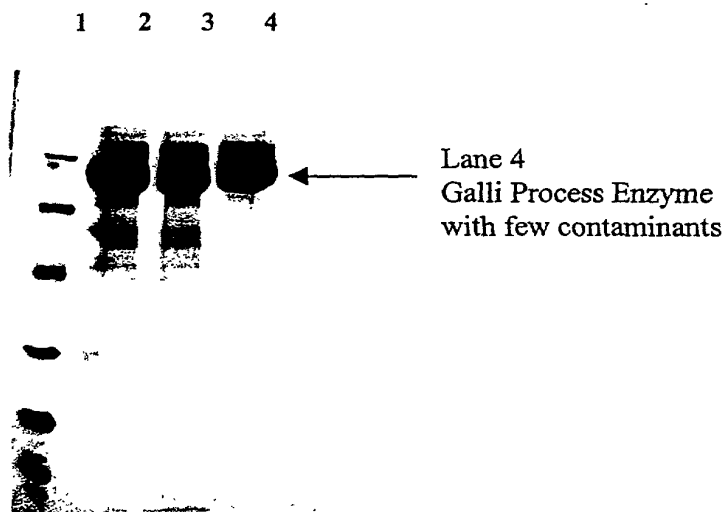
FIGURE 1G

FIGURE 2. SDS-POLYACRYLAMIDE GELS DEMONSTRATING IMPROVEMENTS IN PURITY

Gel using the Kakkis et al 1994, published procedure for purification



Gel using the new Galli Process contained in this application



1. Molecular Weight Marker
2. Prior Process Carson (nonpublished) Batch 2000C9001 Reference Reduced (7.5 µg)
3. Same Batch 2000C9001 Reference Reduced (5.0 µg)
4. Galli Process Enzyme Batch P10006 (5.0 µg)

FIGURE 2

FIGURE 3A IDURONIDASE PRODUCTION USING THE GALLI PROCESS

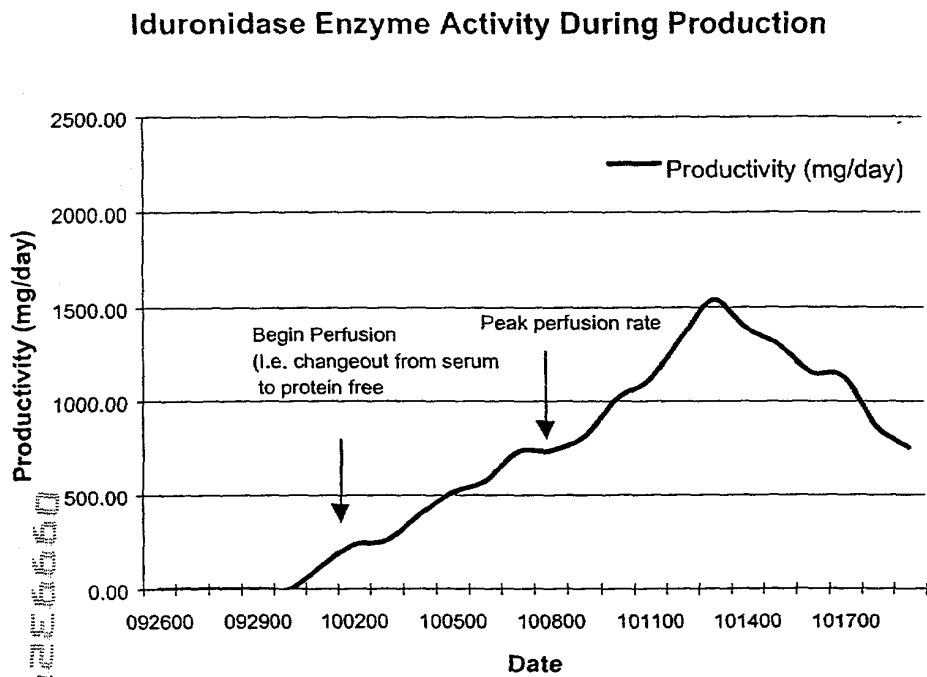
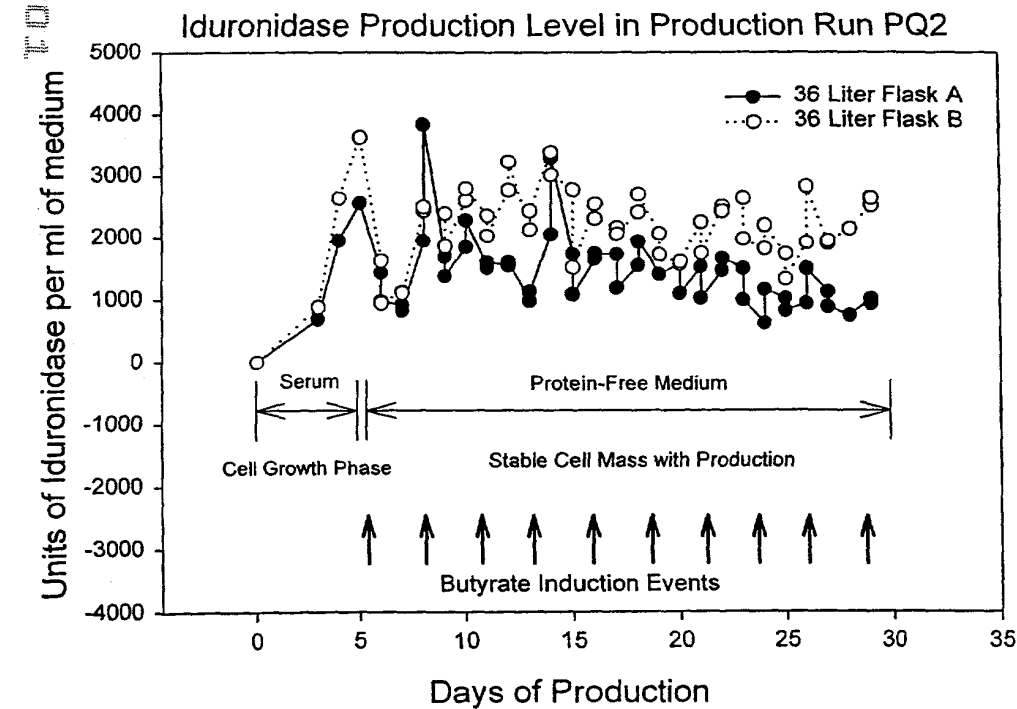


FIGURE 3B. IDURONIDASE PRODUCTION USING BUTYRATE INDUCTION



Reduction in Liver Volume During Enzyme Therapy

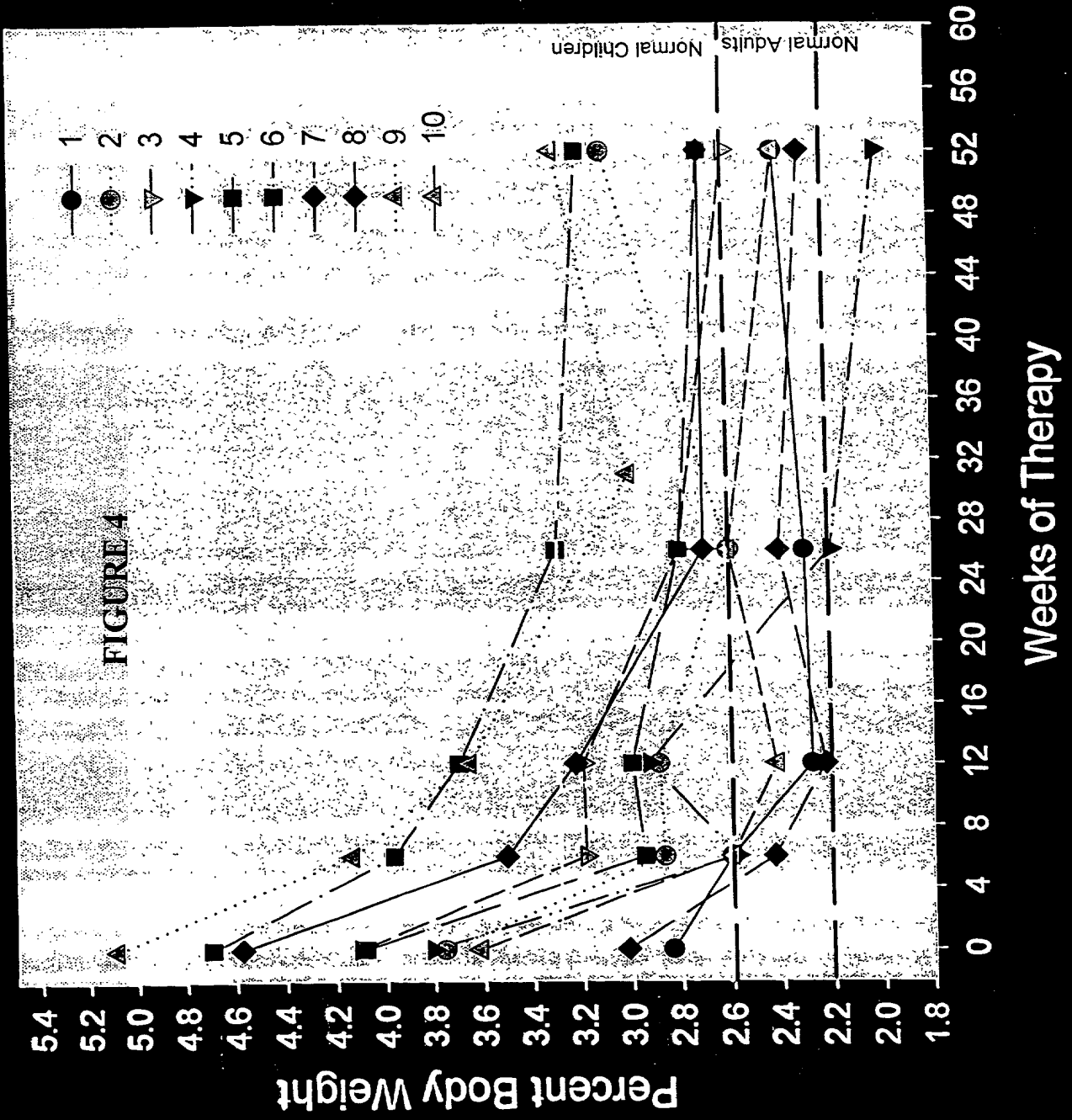


FIGURE 4

Urinary GAG Excretion During Enzyme Therapy

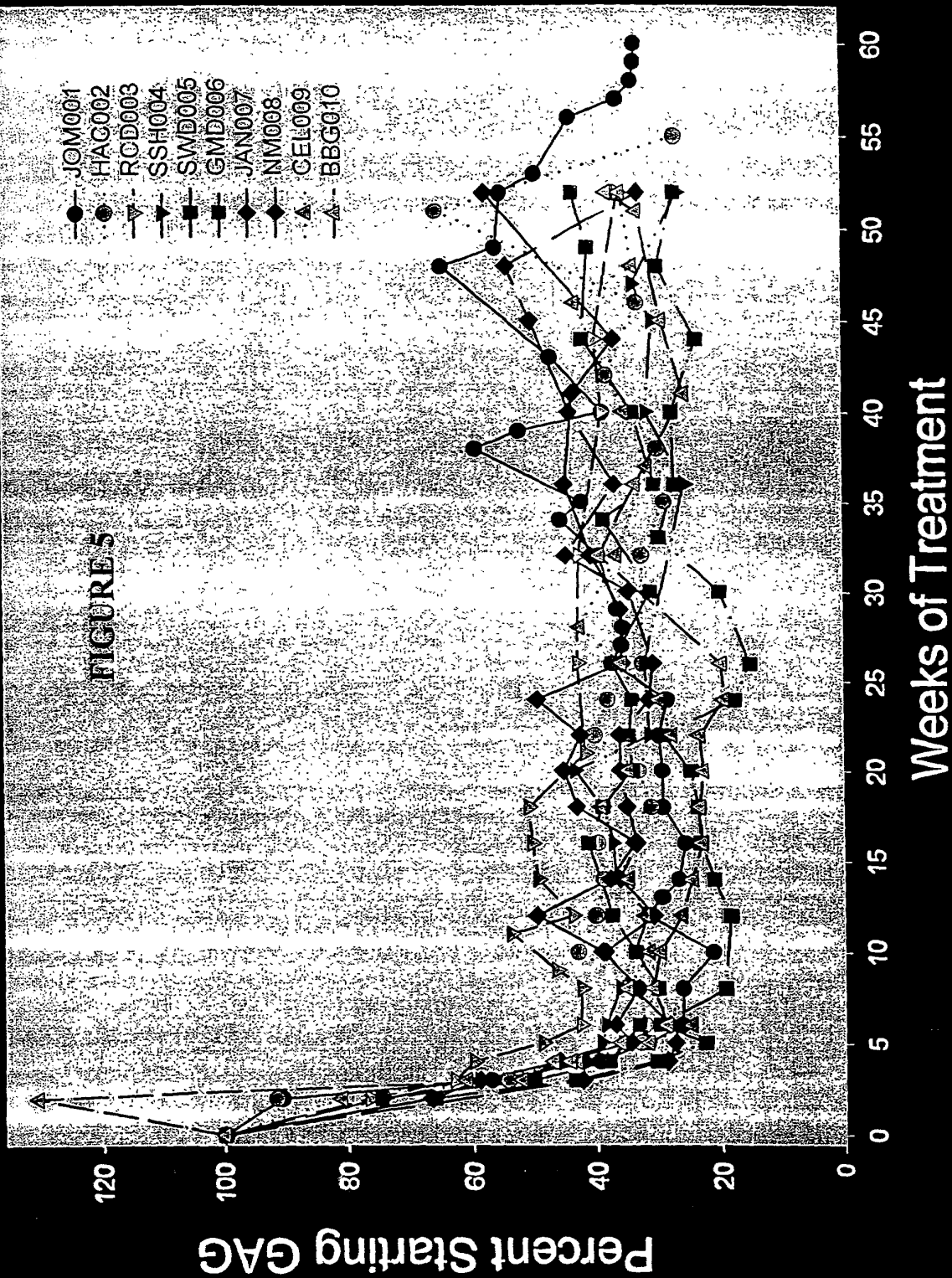


FIGURE 5

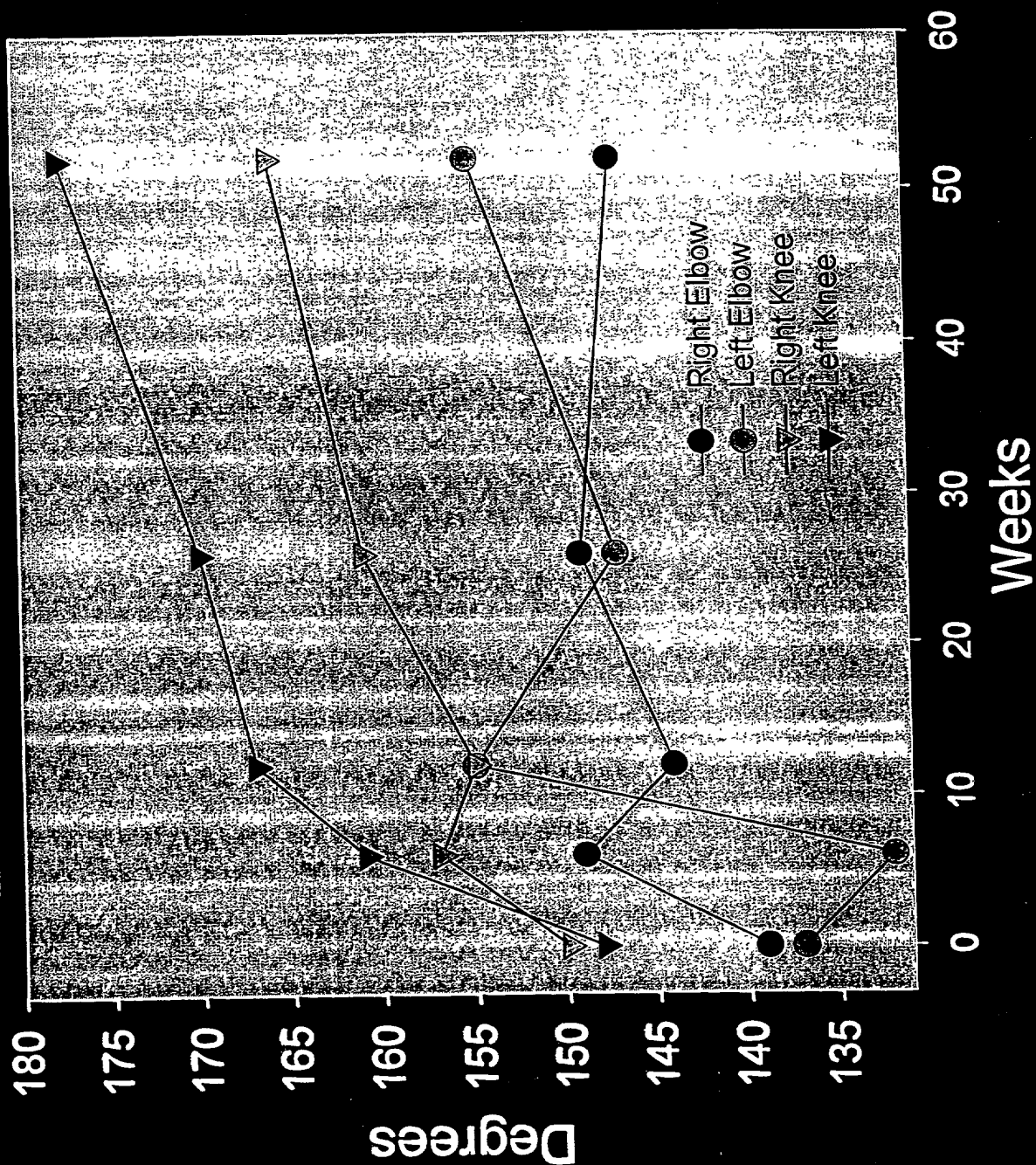


FIGURE 6

Shoulder flexion in four patients with modest restriction

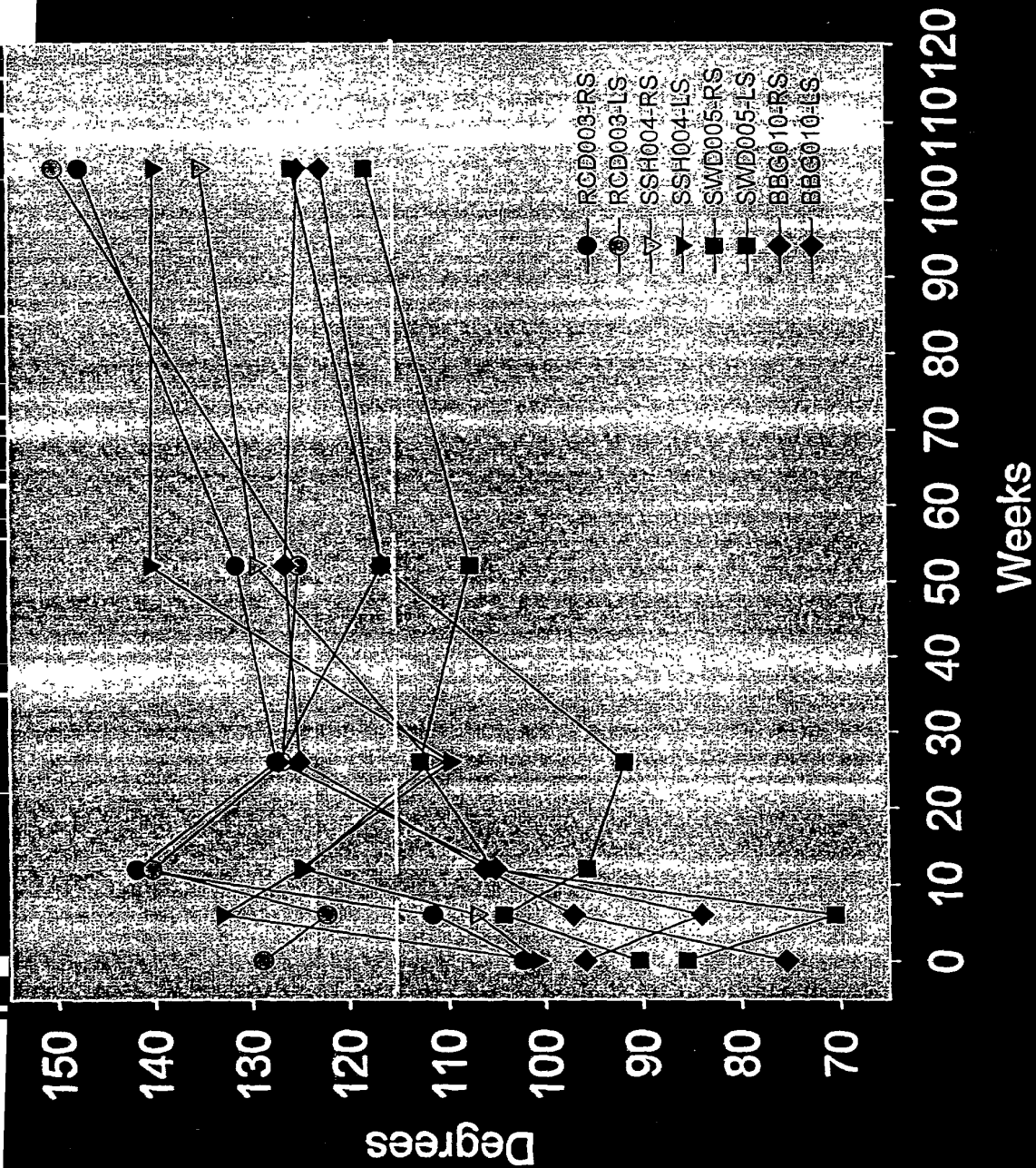


FIGURE 7

Sleep Apnea Improves

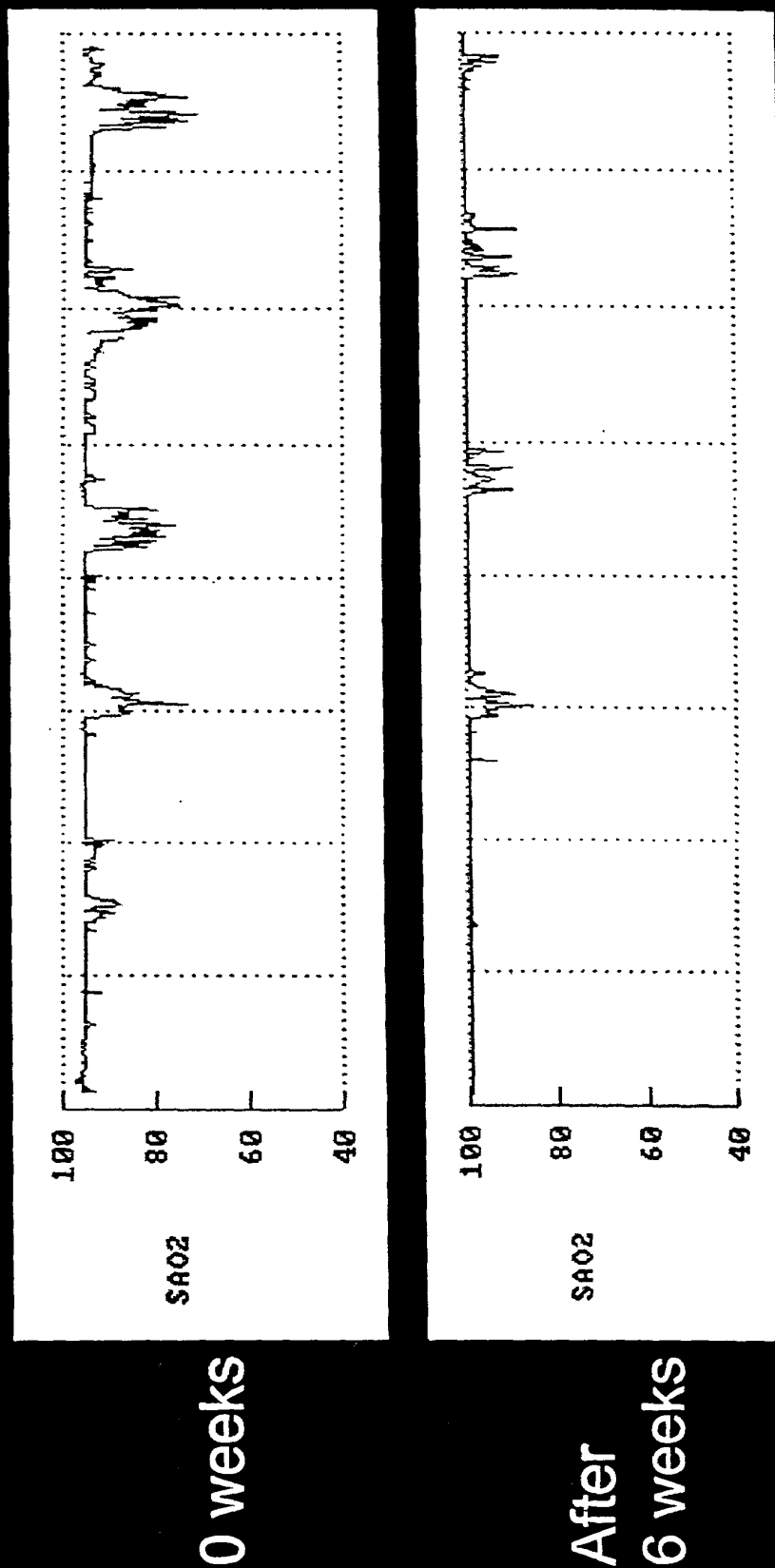
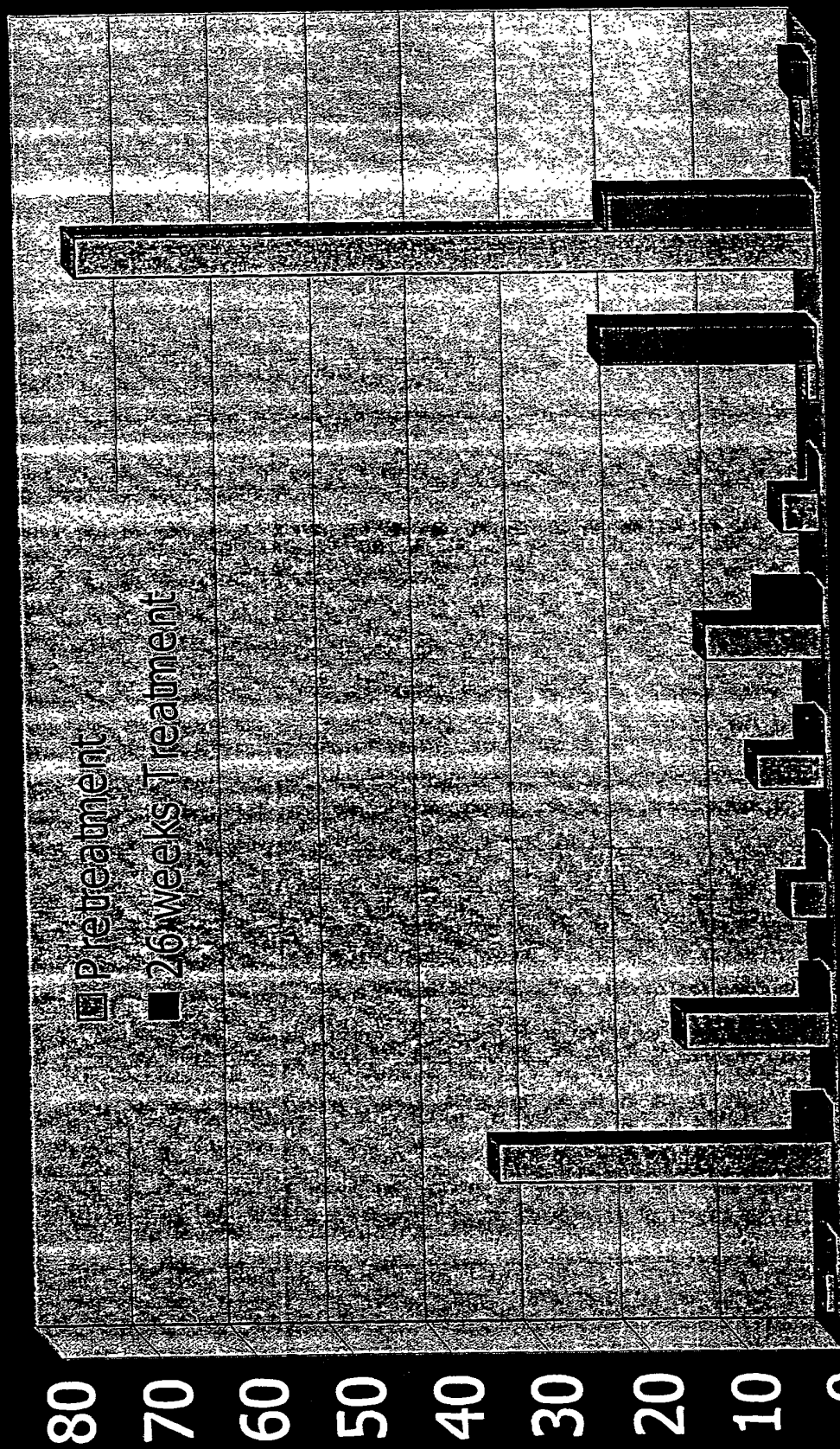


FIGURE 8

Apneas + Hypopneas During Sleep

Pre and Post Treatment



JOM001 AHC002 RCD003 SSH004 SWD005 GMD006 JAN007 N-M008 CEL009 BBG010

FIGURE 9

Pulmonary Function Tests in GIMD006

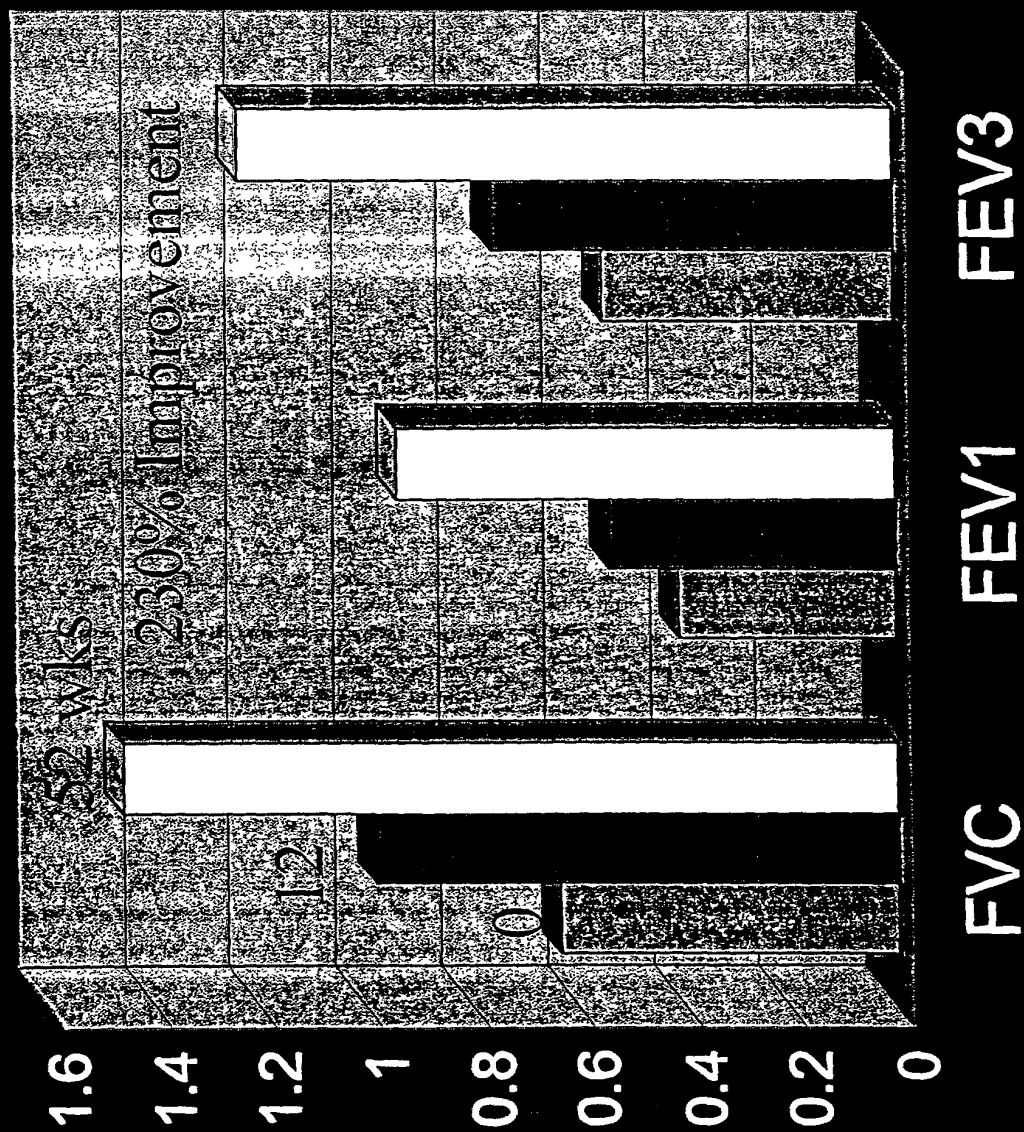


FIGURE 10

Increased Height Growth Velocity

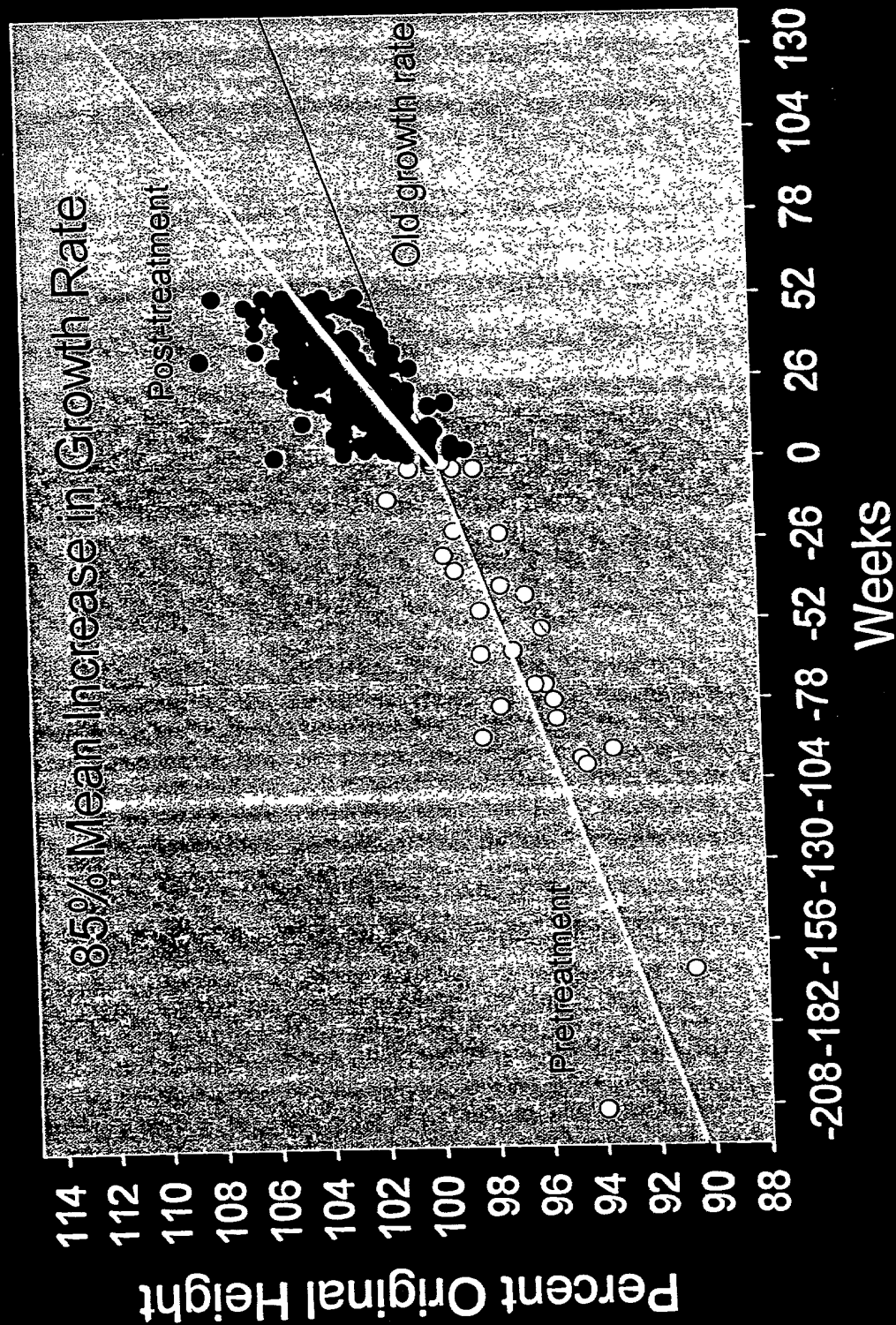


FIGURE 11

FIGURE 12.

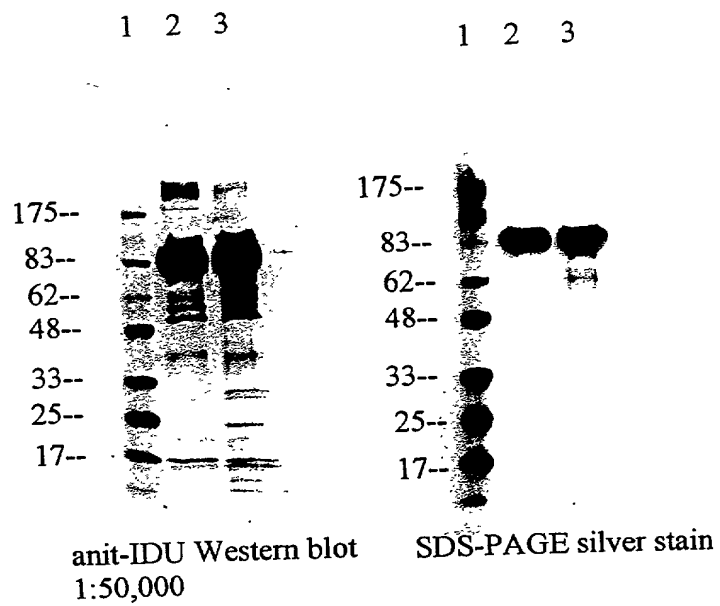
COMPARISON OF HOST PROTEIN CONTAMINATION BETWEEN A PRIOR AND THE NEW GALLI PROCESS

Chinese Hamster Ovary Host Protein Contamination by ELISA Assay

SOURCE AND BATCH NUMBER	CHOP PROTEIN CONTAMINATION (microgram per milligram)	PERCENT CHOP CONTAMINATION	PURITY OF THE ENZYME FROM CHOP
Prior Process (Carson/REI)			
C9002	14	1.4%	98.6%
C9003	24	2.4%	97.6%
C9004	16	1.6%	98.4%
New Process (Galli)			
P1003	<1.3	<0.13%	>99.9%
P1006	1.2	0.12%	99.9%
P1007	<0.6	<0.06%	>99.9%
P1008	<0.67	<0.067%	>99.9%

FIGURE 12

Comparison of Galli and Carson Material



- 1 Marker
- 2 Galli Referenced-0201
- 3 Carson C9002

5ug/lane

FIGURE 13